

Sequence Listing

<110> Baker, Kevin
 Botstein, David
 Eaton, Dan
 Ferrara, Napoleone
 Filvar, ft. Ellen
 Gerbit, en. Mary
 Goddard, Audrey
 Godwki, Paul
 Grimaldi, Christopher
 Gurney, Austin
 Hill, n. Kenneth
 Klavins, Ivar
 Napier, Mary
 Roy, Margaret
 Tumas, Daniel
 Wood, William

<120> SEQUENCED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
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<151> December 1, 1997

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<151> February 28, 2001

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<212> DNA

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cagttctaga ctgtctttct acactaagac accatgaag agtatgtgct 250
ctatttttct ctgttttgt gctctgcaaa accctttctt agcccttcac 300
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gaactatth' a'nttatggg ctgactctga acaacaacaa gctaaccgaag 650
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gtcccaaat caactaagt' aaataacct taatcttccc aaatcattag 750
cagaactcag aattcatgaa aataaagtta agaaaatata aaaggacaca 800

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 atatacaat tgcagagga aaactgact agtttctaa aggtttaca 950
 ccaatttat tggagttta cttagattat aataaaatt caaagtgga 1000
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 attacagag tgaaatcgc tccagtaat ctctcttat tctattaa 1200
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<212> PRT
<213> Homo Sapien

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20 30
Leu Lys Asp Met Glu Asp Thr Asp Asp Asp Asp Asp Asp Asp
35 45
Asp Asp Asp Asp Asp Glu Asp Asn Ser Leu Phe Pro Thr Arg Glu
50 60
Pro Arg Ser His Phe Phe Pro Phe Asp Leu Phe Pro Met Cys Pro
65 75
Phe Gly Cys Gln Cys Tyr Ser Arg Val Val His Cys Ser Asp Leu
80 90
Gly Leu Thr Ser Val Pro Thr Asn Ile Pro Phe Asp Thr Arg Met
100 105
Leu Asp Leu Gln Asn Asn Lys Ile Lys Glu Ile Lys Glu Asn Asp
110 120
Phe Lys Gly Leu Thr Ser Leu Tyr Gly Leu Ile Leu Asn Asn Asn
125 135
Lys Leu Thr Lys Ile His Pro Lys Ala Phe Leu Thr Thr Lys Lys
140 150
Leu Arg Arg Leu Tyr Leu Ser His Asn Gln Leu Ser Glu Ile Pro
155 165
Leu Asn Leu Pro Lys Ser Leu Ala Glu Leu Arg Ile His Glu Asn
170 180
Lys Val Lys Lys Ile Gln Lys Asp Thr Phe Lys Gly Met Asn Ala
185 195
Leu His Val Leu Glu Met Ser Ala Asn Pro Leu Asp Asn Asn Gly
200 210

Ile	Glu	Pro	Gly	Ala	Phe	Glu	Gly	Val	Thr	Val	Phe	His	Ile	Arg	215	22	225
Ile	Ala	Glu	Ala	Lys	Leu	Thr	Ser	Val	Pro	Lys	Gly	Leu	Pro	Pro	230	234	240
Thr	Leu	Leu	Glu	Leu	His	Leu	Asp	Tyr	Asn	Lys	Ile	Ser	Thr	Val	245	250	255
Glu	Leu	Glu	Asp	Phe	Lys	Arg	Tyr	Lys	Glu	Leu	Gln	Arg	Leu	Gly	260	265	270
Leu	Gly	Asn	Asn	Lys	Ile	Thr	Asp	Ile	Glu	Asn	Gly	Ser	Leu	Ala	275	280	285
Asn	Ile	Pro	Arg	Val	Arg	Glu	Ile	His	Leu	Glu	Asn	Asn	Lys	Leu	290	295	300
Lys	Lys	Ile	Pro	Ser	Gly	Leu	Pro	Glu	Leu	Lys	Tyr	Leu	Gln	Ile	305	310	315
Ile	Phe	Leu	His	Ser	Asn	Ser	Ile	Ala	Arg	Val	Gly	Val	Asn	Asp	320	325	330
Phe	Cys	Pro	Thr	Val	Pro	Lys	Met	Lys	Lys	Ser	Leu	Tyr	Ser	Ala	335	340	345
Ile	Ser	Leu	Phe	Asn	Asn	Pro	Val	Lys	Tyr	Trp	Glu	Met	Gln	Pro	350	355	360
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 <213> Artificial Sequence

<220>
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<220>
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 <211> 441
 <212> DNA
 <213> Homo Sapien

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 <213> Homo Sapien

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 35 40 45
 Arg Gly Ala Ala Gly Cys Thr Phe Gly Gly Lys Val Tyr Ala Leu
 50 55 60
 Asp Glu Thr Trp His Pro Asp Leu Gly Gln Pro Phe Gly Val Met
 65 70 75

Arg Cys Val Leu Cys Ala Cys Glu Ala Pro Gln Trp Gly Arg Arg
80 85 90

Thr Arg Gly Pro Gly Arg Val Ser Cys Lys Asn Ile Lys Pro Glu
95 100 105

Cys Pro Thr Pro Ala Cys Gly Gln Pro Arg Gln Leu Pro Gly His
110 115 120

Cys Cys Gln Thr Cys Pro Gln Glu Arg Ser Ser Ser Glu Arg Gln
125 130 135

Pro Ser Gly Leu Ser Phe Glu Tyr Pro Arg Asp Pro Glu His Arg
140 145 150

Ser Tyr Ser Asp Arg Gly Glu Pro Gly Ala Glu Glu Arg Ala Arg
155 160 165

Gly Asp Gly His Thr Asp Phe Val Ala Leu Leu Thr Gly Pro Arg
170 175 180

Ser Gln Ala Val Ala Arg Ala Arg Val Ser Leu Leu Arg Ser Ser
185 190 195

Leu Arg Phe Ser Ile Ser Tyr Arg Arg Leu Asp Arg Pro Thr Arg
200 205 210

Ile Arg Phe Ser Asp Ser Asn Gly Ser Val Leu Phe Glu His Pro
215 220 225

Ala Ala Pro Thr Gln Asp Gly Leu Val Cys Gly Val Trp Arg Ala
230 235 240

Val Pro Arg Leu Ser Leu Arg Leu Leu Arg Ala Glu Gln Leu His
245 250 255

Val Ala Leu Val Thr Leu Thr His Pro Ser Gly Glu Val Trp Gly
260 265 270

Pro Leu Ile Arg His Arg Ala Leu Ala Ala Glu Thr Phe Ser Ala
275 280 285

Ile Leu Thr Leu Glu Gly Pro Pro Gln Gln Gly Val Gly Gly Ile
290 295 300

Thr Leu Leu Thr Leu Ser Asp Thr Glu Asp Ser Leu His Phe Leu
305 310 315

Leu Leu Phe Arg Gly Leu Leu Glu Pro Arg Ser Gly Gly Leu Thr
320 325 330

Gln Val Pro Leu Arg Leu Gln Ile Leu His Gln Gly Gln Leu Leu
335 340 345

Arg Glu Leu Gln Ala Asn Val Ser Ala Gln Glu Pro Gly Phe Ala
350 355 360

Glu Val Leu Pro Asn Leu Thr Val Gln Glu Met Asp Trp Leu Val

365

370

375

Leu Gly Glu Leu Gln Met Ala Leu Glu Trp Ala Gly Arg Pro Gly
380 385 390

Leu Arg Ile Ser Gly His Ile Ala Ala Arg Lys Ser Cys Asp Val
395 400 405

Leu Gln Ser Val Leu Cys Gly Ala Asp Ala Leu Ile Pro Val Gln
410 415 420

Thr Gly Ala Ala Gly Ser Ala Ser Leu Thr Leu Leu Gly Asn Gly
425 430 435

Ser Leu Ile Tyr Gln Val Gln Val Val Gly Thr Ser Ser Glu Val
440 445 450

Val Ala Met Thr Leu Glu Thr Lys Pro Gln Arg Arg Asp Gln Arg
455 460 465

Thr Val Leu Cys His Met Ala Gly Leu Gln Pro Gly Gly His Thr
470 475 480

Ala Val Gly Ile Cys Pro Gly Leu Gly Ala Arg Gly Ala His Met
485 490 495

Leu Leu Gln Asn Glu Leu Phe Leu Asn Val Gly Thr Lys Asp Phe
500 505 510

Pro Asp Gly Glu Leu Arg Gly His Val Ala Ala Leu Pro Tyr Cys
515 520 525

Gly His Ser Ala Arg His Asp Thr Leu Pro Val Pro Leu Ala Gly
530 535 540

Ala Leu Val Leu Pro Pro Val Lys Ser Gln Ala Ala Gly His Ala
545 550 555

Trp Leu Ser Leu Asp Thr His Cys His Leu His Tyr Glu Val Leu
560 565 570

Leu Ala Gly Leu Gly Gly Ser Glu Gln Gly Thr Val Thr Ala His
575 580 585

Leu Leu Gly Pro Pro Gly Thr Pro Gly Pro Arg Arg Leu Leu Lys
590 595 600

Gly Phe Tyr Gly Ser Glu Ala Gln Gly Val Val Lys Asp Leu Glu
605 610 615

Pro Glu Leu Leu Arg His Leu Ala Lys Gly Met Ala Ser Leu Met
620 625 630

Ile Thr Thr Lys Gly Ser Pro Arg Gly Glu Leu Arg Gly Gln Val
635 640 645

His Ile Ala Asn Gln Cys Glu Val Gly Gly Leu Arg Leu Glu Ala
650 655 660

Ala Gly Ala Glu Gly Val Arg Ala Leu Gly Ala Pro Asp Thr Ala
665 670 675

Ser Ala Ala Pro Pro Val Val Pro Gly Leu Pro Ala Leu Ala Pro
680 685 690

Ala Lys Pro Gly Gly Pro Gly Arg Pro Arg Asp Pro Asn Thr Cys
695 700 705

Phe Phe Glu Gly Gln Gln Arg Pro His Gly Ala Arg Trp Ala Pro
710 715 720

Asn Tyr Asp Pro Leu Cys Ser Leu Cys Thr Cys Gln Arg Arg Thr
725 730 735

Val Ile Cys Asp Pro Val Val Cys Pro Pro Pro Ser Cys Pro His
740 745 750

Pro Val Gln Ala Pro Asp Gln Cys Cys Pro Val Cys Pro Glu Lys
755 760 765

Gln Asp Val Arg Asp Leu Pro Gly Leu Pro Arg Ser Arg Asp Pro
770 775 780

Gly Glu Gly Cys Tyr Phe Asp Gly Asp Arg Ser Trp Arg Ala Ala
785 790 795

Gly Thr Arg Trp His Pro Val Val Pro Pro Phe Gly Leu Ile Lys
800 805 810

Cys Ala Val Cys Thr Cys Lys Gly Gly Thr Gly Glu Val His Cys
815 820 825

Glu Lys Val Gln Cys Pro Arg Leu Ala Cys Ala Gln Pro Val Arg
830 835 840

Val Asn Pro Thr Asp Cys Cys Lys Gln Cys Pro Val Gly Ser Gly
845 850 855

Ala His Pro Gln Leu Gly Asp Pro Met Gln Ala Asp Gly Pro Arg
860 865 870

Gly Cys Arg Phe Ala Gly Gln Trp Phe Pro Glu Ser Gln Ser Trp
875 880 885

His Pro Ser Val Pro Pro Phe Gly Glu Met Ser Cys Ile Thr Cys
890 895 900

Arg Cys Gly Ala Gly Val Pro His Cys Glu Arg Asp Asp Cys Ser
905 910 915

Leu Pro Leu Ser Cys Gly Ser Gly Lys Glu Ser Arg Cys Cys Ser
920 925 930

Arg Cys Thr Ala His Arg Arg Pro Pro Glu Thr Arg Thr Asp Pro
935 940 945

Glu Leu Glu Lys Glu Ala Glu Gly Ser

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 <213> Artificial Sequence

<220>
 <221> Synthetic Oligonucleotide probe

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 <212> DNA
 <213> Artificial Sequence

<220>
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<400> 9
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<210> 10
 <211> 36
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<220>
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<400> 12
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<210> 13

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<220>
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 <212> DNA
 <213> Homo Sapien

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 gaaacagcc atggttata atgctactg cccgctggt tgggtggag 1950
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tgtgaaaact atagacgatg ttttaatgta ccttcagtc tetaaactgt 2550
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 ttctttaaaa agtcaagggt tctatattgt gaggtaatta aatttacatt 3050
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 tcagtagtga gtattttctc tagtgcaagt ttattttctt ccaggatggt 3150
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<210> 15
 <211> 717
 <212> PPT
 <213> Homo Sapien

<400> 15
 Met Gln Pro Arg Arg Ala Gln Ala Pro Gly Ala Gln Leu Leu Pro
 1 5 10 15
 Ala Leu Ala Leu Leu Leu Leu Leu Gly Ala Gly Pro Arg Gly
 20 25 30
 Ser Ser Leu Ala Asn Pro Val Pro Ala Ala Pro Leu Ser Ala Pro
 35 40 45
 Gly Pro Cys Ala Ala Gln Pro Cys Arg Asn Gly Gly Val Cys Thr
 50 55 60
 Ser Arg Pro Glu Pro Asp Pro Gln His Pro Ala Pro Ala Gly Gln
 65 70 75
 Pro Gly Tyr Ser Cys Thr Cys Pro Ala Gly Ile Ser Gly Ala Asn
 80 85 90
 Cys Gln Leu Val Ala Asp Pro Cys Ala Ser Asn Pro Cys His His
 95 100 105
 Gly Asn Cys Ser Ser Ser Ser Ser Ser Ser Asp Gly Tyr Leu

	110	115	120
Cys Ile Cys Asn	Glu Gly Tyr Glu Gly	Pro Asn Cys Glu Gln Ala	
	125	130	135
Leu Pro Ser Leu	Pro Ala Thr Gly Trp	Thr Glu Ser Met Ala Pro	
	140	145	150
Arg Gln Leu Gln	Pro Val Pro Ala Thr	Gln Glu Pro Asp Lys Ile	
	155	160	165
Leu Pro Arg Ser	Gln Ala Thr Val Thr	Leu Pro Thr Trp Gln Pro	
	170	175	180
Lys Thr Gly Gln	Lys Val Val Glu Met	Lys Trp Asp Gln Val Glu	
	185	190	195
Val Ile Pro Asp	Ile Ala Cys Gly Asn	Ala Ser Ser Asn Ser Ser	
	200	205	210
Ala Gly Gly Arg	Leu Val Ser Phe Glu	Val Pro Gln Asn Thr Ser	
	215	220	225
Val Lys Ile Arg	Gln Asp Ala Thr Ala	Ser Leu Ile Leu Leu Trp	
	230	235	240
Lys Val Thr Ala	Thr Gly Phe Gln Gln	Cys Ser Leu Ile Asp Gly	
	245	250	255
Arg Ser Val Thr	Pro Leu Gln Ala Ser	Gly Gly Leu Val Leu Leu	
	260	265	270
Glu Glu Met Leu	Ala Leu Gly Asn Asn	His Phe Ile Gly Phe Val	
	275	280	285
Asn Asp Ser Val	Thr Lys Ser Ile Val	Ala Leu Arg Leu Thr Leu	
	290	295	300
Val Val Lys Val	Ser Thr Cys Val Pro	Gly Glu Ser His Ala Asn	
	305	310	315
Asp Leu Glu Cys	Ser Gly Lys Gly Lys	Cys Thr Thr Lys Pro Ser	
	320	325	330
Glu Ala Thr Phe	Ser Cys Thr Cys Glu	Glu Gln Tyr Val Gly Thr	
	335	340	345
Phe Cys Glu Glu	Tyr Asp Ala Cys Gln	Arg Lys Pro Cys Gln Asn	
	350	355	360
Asn Ala Ser Cys	Ile Asp Ala Asn Glu	Lys Gln Asp Gly Ser Asn	
	365	370	375
Phe Thr Cys Val	Cys Leu Pro Gly Tyr	Thr Gly Glu Leu Cys Gln	
	380	385	390
Ser Lys Ile Asp	Tyr Cys Ile Leu Asp	Pro Cys Arg Asn Gly Ala	
	395	400	405

Thr Cys Ile Ser Ser Leu Ser Gly Phe Thr Cys Gln Cys Pro Glu
 41 415 420
 Gly Tyr Phe Gly Ser Ala Cys Glu Glu Lys Val Asp Pro Cys Ala
 425 430 435
 Ser Ser Pro Cys Gln Asn Asn Gly Thr Cys Tyr Val Asp Gly Val
 440 445 450
 His Phe Thr Cys Asn Cys Ser Pro Gly Phe Thr Gly Pro Thr Cys
 455 460 465
 Ala Gln Leu Ile Asp Phe Cys Ala Leu Ser Pro Cys Ala His Gly
 470 475 480
 Thr Cys Arg Ser Val Gly Thr Ser Tyr Lys Cys Leu Cys Asp Pro
 485 490 495
 Gly Tyr His Gly Leu Tyr Cys Glu Glu Glu Tyr Asn Glu Cys Leu
 500 505 510
 Ser Ala Pro Cys Leu Asn Ala Ala Thr Cys Arg Asp Leu Val Asn
 515 520 525
 Gly Tyr Glu Cys Val Cys Leu Ala Glu Tyr Lys Gly Thr His Cys
 530 535 540
 Glu Leu Tyr Lys Asp Pro Cys Ala Asn Val Ser Cys Leu Asn Gly
 545 550 555
 Ala Thr Cys Asp Ser Asp Gly Leu Asn Gly Thr Cys Ile Cys Ala
 560 565 570
 Pro Gly Phe Thr Gly Glu Glu Cys Asp Ile Asp Ile Asn Glu Cys
 575 580 585
 Asp Ser Asn Pro Cys His His Gly Gly Ser Cys Leu Asp Gln Pro
 590 595 600
 Asn Gly Tyr Asn Cys His Cys Pro His Gly Trp Val Gly Ala Asn
 605 610 615
 Cys Glu Ile His Leu Gln Trp Lys Ser Gly His Met Ala Glu Ser
 620 625 630
 Leu Thr Asn Met Pro Arg His Ser Leu Tyr Ile Ile Ile Gly Ala
 635 640 645
 Leu Cys Val Ala Phe Ile Leu Met Leu Ile Ile Leu Ile Val Gly
 650 655 660
 Ile Cys Arg Ile Ser Asn Ile Glu Tyr Gln Gly Ser Ser Arg Pro
 665 670 675
 Ala Tyr Glu Glu Phe Tyr Asn Cys Arg Ser Ile Asp Ser Glu Phe
 680 685 690
 Ser Asn Ala Ile Ala Ser Ile Arg His Ala Arg Phe Gly Lys Lys

695

700

705

Ser Arg Pro Ala Met Tyr Asp Val Ser Pro Ile Ala Tyr Glu Asp
710 715 720

Tyr Ser Pro Asp Asp Lys Pro Leu Val Thr Leu Ile Lys Thr Lys
725 730 735

Asp Leu

<210> 16

<211> 43

<212> DNA

<213> Artificial Sequence

<220>

<221> Synthetic Oligonucleotide Probe

<400> 16

tgtaaaacga cggccagtta aatagaacctg caattattaa tct 43

<210> 17

<211> 41

<212> DNA

<213> Artificial Sequence

<220>

<221> Synthetic Oligonucleotide Probe

<400> 17

caaggaaacag ctatgaccac ctgcacacct gcaaatccat t 41

<210> 13

<211> 508

<212> DNA

<213> Homo Sapien

<400> 13

ctctgggaagg tcaaggccac aggatcccaa cagtgcctcc tcatagatgg 50
atgaaaagtgt gacccccctt tcaggctttc aggggggaactg gtctctcttg 100
atgagatgct cgccttgggg aataatcaat ttattggttt tgtgaatgat 150
tctgtgaacta agtctattgt ggttttgccc ttaactctgg tggagaaggt 200
cagcaacctgt gtgccggggg agagtcacgc aaatgaacttg gagtgttcag 250
gaaaaaggaaa atgcaccacg aagccgtcag aggcacattt ttctgtacc 300
tgtgaagagc agtactgtgg tactttctgt gaagatatac atgcttgcca 350
gaggaaacat tgcacaaaca accggagctg tattgatgca aatgaaaagc 400
aagatgggag caatttcacc tgtgtttgac ttctgggta tactggagag 450
ctttgcacac cgaactgaga ttggagcgaa cgacctacac cgaactgaga 500

tagggag 508

<210> 19
<211> 508
<212> DNA
<213> Homo Sapien

<400> 1
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acataagtgt gaccccccctt taaggctttc aggggactg atcctctat 100
aggagatgct cgccttgggg aataatcact ttattgggtt tctgaatgat 150
tcttgarta agtctattgt ggctttgggc ttaactctgg tggggaaggt 200
cagcaactgt gtgcgggggg agagtcacgc aaatgacttg gagtgttcag 250
gaaaaggaaa atgcaccacg aagccgtcag aggaacttt ttctgtacc 300
tgtgagagc agtacgtggg taactttctgt gaagaatacg atgcttgcca 350
gaggaaacct tgccaaaaa aaggagctg tattgatgca aatgaaaagc 400
aagatggag caatttcacc tgtgtttgcc ttctgtgta tactggagag 450
ctttgcacac cgaactgaga ttggagcgaa cgacctacac cgaactgaga 500

ttagggag 508

<210> 20
<211> 21
<212> RNA
<213> Artificial Sequence

<220>
<221> Synthetic Oligonucleotide Probe

<400> 10
cttctgaagg tcaaggccac agg 21

<210> 11
<211> 14
<212> DNA
<213> Artificial Sequence

<220>
<221> Synthetic oligonucleotide probe

<400> 21
ctcagttcgg ttggcaaaag tctc 24

<210> 22
<211> 69
<212> DNA
<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 22

cagtgtctccc tcatagatgg acgaaagtgt gacccccctt tcaggcgaga 50

gttttgaaa cgaactga 69

<210> 21

<211> 1920

<212> DNA

<213> Homo Sapien

<410> 23

gtttagtctg ctgtctctg tctctctgt ccagcttga acctgtgctt 50

atatacggc agggccccc agagctctc ccacgtggg cggcccccaga 100

ggcccaccc ttgagggaac ctactctcc tcjaccacac tcajtagtcc 150

cagatccac ggcctgcaag agcagggaag gcccctgatg cgggaacttc 200

cgtctgttga cggccacacac gacctggccc tggctctaac gcaaggtttac 250

cagaaagggc tacaggatgt taacttgcgc aatttcagct atggccagac 300

cagcttggaac aggttagag atggctcgt gggcgccag ttctggtcag 350

ctatgttgc ataccagacc caggaccggg atgcccctgg ctccacctg 400

ttgcagattg acctctaac ccgcatgtgt gctctctatt ctgagcttga 450

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aacggctgg gcatgatgtt agacttacc catgtctcag atgttgttgc 750

atgggggac ctggaagtgt cacaggcacc tctgtcttc tccacttgg 800

ctggccgggg ttgttgcaac agtgtctga atgttctga tgacatctg 850

caacttctga aaaaagaagg ttgctgtgt atgtgtctt tgtccatggg 900

agtaatacag tgcacccat caaccaatgt gtcacatgtg gacatcact 950

tgcacacat ctatgtgtc atttgatcca agttracgg catttggtga 1000

gattatgatg gggcgggaaa attccctcag gggctggaag acctgtctac 1050

ataccgggtc ctgatagagg agttgtgag tctgtcctgg agtgagggaag 1100

agtttcaggg tgtccttctt ggaaacctgc tgcgggtctt cagacaagtg 1150

Asn Asn Ile Ser Gly Leu Thr Asp Phe Gly Glu Lys Val Val Ala
185 190 195

Glu Met Asn Arg Leu Gly Met Met Val Asp Leu Ser His Val Ser
200 205 210

Asp Ala Val Ala Arg Arg Ala Leu Glu Val Ser Gln Ala Pro Val
215 220 225

Ile Phe Ser His Ser Ala Ala Arg Gly Val Cys Asn Ser Ala Arg
230 235 240

Asn Val Pro Asp Asp Ile Leu Gln Leu Ile Lys Lys Asn Gly Gly
245 250 255

Val Val Met Val Ser Leu Ser Met Gly Val Ile Gln Cys Asn Pro
260 265 270

Ser Ala Asn Val Ser Thr Val Ala Asp His Phe Asp His Ile Lys
275 280 285

Ala Val Ile Gly Ser Lys Phe Ile Gly Ile Gly Gly Asp Tyr Asp
290 295 300

Gly Ala Gly Lys Phe Pro Gln Gly Leu Gln Asp Val Ser Thr Tyr
305 310 315

Pro Val Leu Ile Glu Glu Leu Leu Ser Arg Gly Trp Ser Glu Glu
320 325 330

Glu Leu Gln Gly Val Leu Arg Gly Asn Leu Leu Arg Val Phe Arg
335 340 345

Gln Val Glu Lys Val Gln Glu Glu Asn Lys Trp Gln Ser Pro Leu
350 355 360

Glu Asp Lys Phe Pro Asp Glu Gln Leu Ser Ser Ser Cys His Ser
365 370 375

Asp Leu Ser Arg Leu Arg Gln Arg Gln Ser Leu Thr Ser Gly Gln
380 385 390

Glu Leu Thr Glu Ile Pro Ile His Trp Thr Ala Lys Leu Pro Ala
395 400 405

Lys Trp Ser Val Ser Glu Ser Ser Pro His Met Ala Pro Val Leu
410 415 420

Ala Val Val Ala Thr Phe Pro Val Leu Ile Leu Trp Leu
425 430

<210> 25

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 25
aggtctgtgtc agcctatgtg cc 22

<210> 26
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<221> Synthetic oligonucleotide probe

<400> 26
cgtgatgggtg tctttgtccc tggg 24

<210> 27
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<221> Synthetic oligonucleotide probe

<400> 27
ctccaccaat ccgatgaac ttgg 24

<210> 28
<211> 50
<212> DNA
<213> Artificial Sequence

<220>
<221> Synthetic oligonucleotide probe

<400> 28
cagcagattg acctcatacg ccgatgtgt gctctctatt ctgagctgga 50

<210> 29
<211> 1416
<212> DNA
<213> Homo Sapien

<400> 29
aaaactata aatattccgg attattcata ccgtcccacc atcgggcqcg 50
gacccggggc cgcgaattct aaaccaacat gcggggcacc tacgtccct 100
cgaaccact cagtagtccc agcaccacgg gcttgcgaaga gcaggcacgg 150
gacctgatgc gggacttccc gctcgtggac ggcacaaag acctgccct 200
ggtcctaaag caggtttacc agaaagggt acaggatgtt aacctggcca 250
atttcagcta cggccagacc agcctcgaca ggttagaga tggcctcgtg 300
ggggcccagt tctggtcagg ctatgtgcca tgcagaccc agyaccggga 350
tgccctgcgc ctcaacctgg agcagattga cctcatacgc ccgatgtgtg 400

cctctctatc tgagctggag cttgtgacct cggctaaage tctgaacgac 450
 actcagaaat tggcctgacct catcgggtgta gagggtggcc actcgttggg 500
 caatagcttc tcatctcttae ctaccttcta catgctggga gtggaatacc 550
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 actcactjag attccatca actggacgc caagttacca gccaagtgt 1300
 caatctcaga ctctcccc cactctgaca aaactcacac atgcccacg 1350
 tggcagcac ctgaactct ggggggacgg tcagtcttcc tcttcccccc 1400
 aaaaaccaag gacacc 1416

<210> 30
 <211> 446
 <212> FRT
 <213> Homo Sapien

<400> 30
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 1 5 10 15
 Thr Gln Gly Leu Gln Gln Gln Ala Arg Ala Leu Met Arg Asp Phe
 20 25 30
 Pro Leu Val Asp Gly His Asn Asp Leu Pro Leu Val Leu Arg Gln
 35 40 45
 Val Tyr Gln Lys Gly Leu Gln Asp Val Asn Leu Arg Asn Phe Ser

50

55

60

Tyr Gly Gln Thr Ser Leu Asp Arg Leu Arg Asp Gly Leu Val Gly
65 70 75

Ala Gln Phe Trp Ser Ala Tyr Val Pro Cys Gln Thr Gln Asp Arg
80 85 90

Asp Ala Leu Arg Leu Thr Leu Gln Gln Ile Asp Leu Ile Arg Arg
95 100 105

Met Cys Ala Ser Tyr Ser Glu Leu Glu Leu Val Thr Ser Ala Lys
110 115 120

Ala Leu Asn Asp Thr Gln Lys Leu Ala Cys Leu Ile Gly Val Glu
125 130 135

Gly Gly His Ser Leu Asp Asn Ser Leu Ser Ile Leu Arg Thr Phe
140 145 150

Tyr Met Leu Gly Val Arg Tyr Leu Thr Leu Thr His Thr Cys Asn
155 160 165

Thr Pro Trp Ala Glu Ser Ser Ala Lys Gly Val His Ser Phe Tyr
170 175 180

Asn Asn Ile Ser Gly Leu Thr Asp Phe Gly Glu Lys Val Val Ala
185 190 195

Glu Met Asn Arg Leu Gly Met Met Val Asp Leu Ser His Val Ser
200 205 210

Asp Ala Val Ala Arg Arg Ala Leu Glu Val Ser Gln Ala Pro Val
215 220 225

Ile Phe Ser His Ser Ala Ala Arg Gly Val Cys Asn Ser Ala Arg
230 235 240

Asn Val Pro Asp Asp Ile Leu Gln Leu Leu Lys Lys Asn Gly Gly
245 250 255

Val Val Met Val Ser Leu Ser Met Gly Val Ile Gln Cys Asn Pro
260 265 270

Ser Ala Asn Val Ser Thr Val Ala Asp His Phe Asp His Ile Lys
275 280 285

Ala Val Ile Gly Ser Lys Phe Ile Gly Ile Gly Gly Asp Tyr Asp
290 295 300

Gly Ala Gly Lys Phe Pro Gln Gly Leu Glu Asp Val Ser Thr Tyr
305 310 315

Pro Val Leu Ile Glu Glu Leu Leu Ser Arg Gly Trp Ser Glu Glu
320 325 330

Glu Leu Gln Gly Val Leu Arg Gly Asn Leu Leu Arg Val Phe Arg
335 340 345

Gln Val Glu Lys Val Gln Glu Glu Asn Lys Trp Gln Ser Pro Leu
350 355 360
Glu Asp Lys Phe Pro Asp Glu Gln Leu Ser Ser Ser Cys His Ser
365 370 375
Asp Leu Ser Arg Leu Arg Gln Arg Gln Ser Leu Thr Ser Gly Gln
380 385 390
Glu Leu Thr Glu Ile Pro Ile His Trp Thr Ala Lys Leu Pro Ala
395 400 405
Lys Trp Ser Val Ser Glu Ser Ser Pro His Pro Asp Lys Thr His
410 415 420
Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser
425 430 435
Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr
440 445

<210> 31
<211> 1795
<212> DNA
<213> Homo Sapien

<400> 31
cyccacagca cgtgaggag gactggccc cgcctccag cgcacggact 50
gagtcacag cctgaccca ccgcagcca gccacagcc gcgcgggac 100
ccggagagc ccgacccat gacgacgc cgcgggggc ccgcaccca 150
atccggagg cggcggcgc cttgatgcc cctgtgtg ctgctctgg 200
tcctgggga gccgcagcc gcatcaggag ccacacaga tatgatcgt 250
ccacagatc ccagcttct cctcgctcc tccgtgtg ccacgtgct 300
agtcacgga gacccacg gacccacc ccagggcctc tactggacc 350
tcaaggggc ccgtgtgcc cctgagctt ccgtgtact caacgcttc 400
acctggctc tggcctgga cacttcaat gattccagg agcggtcgg 450
ggaaacctc gtgtgcaag cctgtgacg caacatcct gctggctct 500
gctctatgt tgcccgcc ccagagaaac ccgtcaacat cagctgctg 550
tccaggaac tgaagactt gacctgggc tggacgac ggcacacgg 600
ggaaacctc ctccacaa actactcct caatcacag cttagatgt 650
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tgccatccc ccaggacct ggtctcttt acgcctatg agatctggg 750
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atatactgga tgtggtgacc acggaccccc cggccgacgt gaacgtgagc 850
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 gaggcactc tgggtgac ccagtggt gtgtgtgt gtg'gaggt 1600
 tgggtggt cctcagac ccagtggt ctgggtgtg gaaggggagt 1650
 cattaacct cattaacct ggccttcca aagagctct tttaaataa 1700
 tgagctattt aggtgtctg atgtgaaaa aaaaaaaaa aaaaaaaaa 1750
 aaaaaaaaa aaaaaaaaa aaaaaaataa aaaaaaaaa 1790

<210> 32
 <211> 412
 <212> FFT
 <213> Homo Sapien

<401> 3.
 Met Pro Ala Gly Arg Arg Gly Pro Ala Ala Gln Ser Ala Arg Arg
 1 5 10 15
 Pro Pro Pro Leu Leu Pro Leu Leu Leu Leu Leu Cys Val Leu Gly
 20 25 30
 Ala Pro Arg Ala Gly Ser Gly Ala His Thr Ala Val Ile Ser Pro
 35 40 45
 Gln Asp Pro Thr Leu Leu Ile Gly Ser Ser Leu Leu Ala Thr Cys
 50 55 60

Ser Val His Gly Asp Pro Pro Gly Ala Thr Ala Glu Gly Leu Tyr
65 70 75

Trp Thr Leu Asn Gly Arg Arg Leu Pro Pro Glu Leu Ser Arg Val
80 85 90

Leu Asn Ala Ser Thr Leu Ala Leu Ala Leu Ala Asn Leu Asn Gly
95 100 105

Ser Arg Gln Arg Ser Gly Asp Asn Leu Val Cys His Ala Arg Asp
110 115 120

Gly Ser Ile Leu Ala Gly Ser Cys Leu Tyr Val Gly Leu Pro Pro
125 130 135

Glu Lys Pro Val Asn Ile Ser Cys Trp Ser Lys Asn Met Lys Asp
140 145 150

Leu Thr Cys Arg Trp Thr Pro Gly Ala His Gly Glu Thr Phe Leu
155 160 165

His Thr Asn Tyr Ser Leu Lys Tyr Lys Leu Arg Trp Tyr Gly Gln
170 175 180

Asp Asn Thr Cys Glu Glu Tyr His Thr Val Gly Pro His Ser Cys
185 190 195

His Ile Pro Lys Asp Leu Ala Leu Phe Thr Pro Tyr Glu Ile Trp
200 205 210

Val Glu Ala Thr Asn Arg Leu Gly Ser Ala Arg Ser Asp Val Leu
215 220 225

Thr Leu Asp Ile Leu Asp Val Val Thr Thr Asp Pro Pro Pro Asp
230 235 240

Val His Val Ser Arg Val Gly Gly Leu Glu Asp Gln Leu Ser Val
245 250 255

Arg Trp Val Ser Pro Pro Ala Leu Lys Asp Phe Leu Phe Gln Ala
260 265 270

Lys Tyr Gln Ile Arg Tyr Arg Val Glu Asp Ser Val Asp Trp Lys
275 280 285

Val Val Asp Asp Val Ser Asn Gln Thr Ser Cys Arg Leu Ala Gly
290 295 300

Leu Lys Pro Gly Thr Val Tyr Phe Val Gln Val Arg Cys Asn Pro
305 310 315

Phe Gly Ile Tyr Gly Ser Lys Lys Ala Gly Ile Trp Ser Glu Trp
320 325 330

Ser His Pro Thr Ala Ala Ser Thr Pro Arg Ser Glu Arg Pro Gly
335 340 345

Pro Gly Gly Gly Ala Cys Glu Pro Arg Gly Gly Glu Pro Ser Ser

350	355	360
Gly Pro Val Arg Arg Glu Leu Lys Gln Phe Leu Gly Trp Leu Lys		
365	370	375
Lys His Ala Tyr Cys Ser Asn Leu Ser Phe Arg Leu Tyr Asp Gln		
380	385	390
Trp Arg Ala Trp Met Gln Lys Ser His Lys Thr Arg Asn Gln Asp		
395	400	405
Glu Gly Ile Leu Pro Ser Gly Arg Arg Gly Thr Ala Arg Gly Pro		
410	415	420
Ala Arg		

<210> 33
 <211> 23
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> Synthetic oligonucleotide probe

<400> 33
 cccgcccgac gtgcacgtga gcc 23

<210> 34
 <211> 23
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> Synthetic oligonucleotide probe

<400> 34
 tgagccagcc caggaactgc ttg 23

<210> 35
 <211> 50
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> Synthetic oligonucleotide probe

<400> 35
 ctagtgcgct gcaaccctt tggcatctat ggtccaaga aagcgggat 50

<210> 36
 <211> 1771
 <212> DNA
 <213> Homo Sapien

<400> 36
 cccaagcgtc cgctggtgtt agatcgagca accctctaaa agcagtttag 50

agtggtaaaa aaaaaaaaaa acacacccaaa cgtctgcagc cacaaaaagg 100
 atgaaatttc ttctggacat cctcctgctt ctcccgttac tgatcgttg 150
 ctccctagag tcttctgtga agctttttat tcttaagagg agaaaaatag 200
 tcaacgaga aatcgtctcg attacaggag ctgcacatgg aattgggaga 250
 ctactgct atgaattgc taaacttaaa agcaagctag ttctctggga 300
 tatataag catgaa tgg aggaacagc tcttaattg aaggaattg 350
 gtgcacaggt ttaactttt gttgttagct gtagcaacg aagagttatt 400
 taagatttg caagaggg gaagcgagaa attggagag ttggtatttt 450
 agtaataat gtgtgttag tctatacctc aattttgtt gctacacaag 500
 atctcagat tgaacagact tttcaagtta atgtacttg acatttttgg 550
 actacaaagg cttttcttc tgcattgag aagaatact atggcctat 600
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 cttactgttc aagcaagttt gctgctgttg gatttcataa aactttgaca 700
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 tcttaattt gtataactg ccttcaccaa aatcgaat caaattttgg 800
 gacacactc ggaactgag gaattggtta acaggcttat gcatggatt 850
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 cccattttt tcaatattat tttgagggt ttggcagttt cactttacta 1150
 ccattgttc tttagcaca agtgattac atatatata aacagagaaa 1200
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 agaacttca agctctctaa ataaatgaa ggactatct tagtggatt 1450
 tcaaatgaa tatcatgac tctcaatggg taggtttcat cctacccatt 1500

gccactctgt ttctgagag atacctcaca ttccaatgcc aaacatttct 1550
 gctaggggaa gctagaggtg gatacaegtg ttgcaagtat aaaagcatca 1600
 ctggattta aggagaattg agagaatgta cccacaaatg gcagcaataa 1650
 taatggatc acacttaaaa aaaaaaaa aaaaaaaa aaaaaaaa 1700
 aaaaaaaa aaaaaaaa aaaaaaaa aaaaaaaa aaaaaaaa 1750
 aaaaaaaa aaaaaaaa a 1771

<110> 17
 <111> 390
 <112> 1FT
 <113> Homo Sapien

<400> 17
 Met Lys Phe Leu Leu Asp Ile Leu Leu Leu Leu Pro Leu Leu Ile
 1 5 10 15
 Val Cys Ser Leu Glu Ser Phe Val Lys Leu Phe Ile Pro Lys Arg
 20 25 30
 Arg Lys Ser Val Thr Gly Glu Ile Val Leu Ile Thr Gly Ala Gly
 35 40 45
 His Gly Ile Gly Arg Leu Thr Ala Tyr Glu Phe Ala Lys Leu Lys
 50 55 60
 Ser Lys Leu Val Leu Trp Asp Ile Asn Lys His Gly Leu Glu Glu
 65 70 75
 Thr Ala Ala Lys Cys Lys Gly Leu Gly Ala Lys Val His Thr Phe
 80 85 90
 Val Val Asp Cys Ser Asn Arg Glu Asp Ile Tyr Ser Ser Ala Lys
 95 100 105
 Lys Val Lys Ala Glu Ile Gly Asp Val Ser Ile Leu Val Asn Asn
 110 115 120
 Ala Gly Val Val Tyr Thr Ser Asp Leu Phe Ala Thr Gln Asp Pro
 125 130 135
 Gln Ile Glu Lys Thr Phe Glu Val Asn Val Leu Ala His Phe Trp
 140 145 150
 Thr Thr Lys Ala Phe Leu Pro Ala Met Thr Lys Asn Asn His Gly
 155 160 165
 His Ile Val Thr Val Ala Ser Ala Ala Gly His Val Ser Val Pro
 170 175 180
 Phe Leu Leu Ala Tyr Cys Ser Ser Lys Phe Ala Ala Val Gly Phe
 185 190 195
 His Lys Thr Leu Thr Asp Glu Leu Ala Ala Leu Gln Ile Thr Gly

200	205	210
Val Lys Thr Thr Cys Leu Cys Pro Asn Phe Val Asn Thr Gly Phe		
215	220	225
Ile Lys Asn Pro Ser Thr Ser Leu Gly Pro Thr Leu Glu Pro Glu		
230	235	240
Glu Val Val Asn Arg Leu Met His Gly Ile Leu Thr Glu Gln Lys		
245	250	255
Met Ile Phe Ile Pro Ser Ser Ile Ala Phe Leu Thr Thr Leu Glu		
260	265	270
Arg Ile Leu Pro Glu Arg Phe Leu Ala Val Leu Lys Arg Lys Ile		
275	280	285
Ser Val Lys Phe Asp Ala Val Ile Gly Tyr Lys Met Lys Ala Gln		
290	295	300

<210> 38

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<221> Synthetic oligonucleotide probe

<400> 38

gggtgaaggca gaaattggag atg 23

<210> 39

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<221> Synthetic oligonucleotide probe

<400> 39

atcccatgca tcagctgtt tacc 24

<210> 40

<211> 48

<212> DNA

<213> Artificial Sequence

<220>

<221> Synthetic oligonucleotide probe

<400> 40

gctgggtgtag tctatcacat agatttgitt gctacacaa atctctat 48

<210> 41

<211> 1377

<212> DNA

<213> Homo Sapien

<400> 41

gaatagtttt ettggagttt gggaggagga aagcggagcc ggcaggagcc 50
gaaccaggac tggggtgacg gcagggcagg gggcgctctg ccgggagaa 100
ggggggggg tggagcaca caactggag ggtcggagt agcagagcc 150
ctgaggggg cctcgggga gccggagg ggggttga gaggagccg 200
gactcgggc tccgggtgc agactatga gggactct catctctg 250
ctcctgggc tggggcgag ctgagcca ctgagaca acaagtcc 300
cagctctgc ccggggga cc cgggttcc aggcacccg ggcacatg 350
ggagccaggg ctggcgagg ccggaggcc ggagggagc ggcaggggc 400
cgggggtt caggagaa ca aggcgggc gggaggagc gactcggg 450
actcgggg gaccgggc cggagagc gggggagc ggggggcca 500
cgggggtg cgggggtg ccgtcttc cgggttcc ctctggcc 550
aagggtccg agagccggg gctcggccg tctgagcc ccttggctt 600
cggcggtg ctggtgagc aaggggga ttacggcc gtcaggga 650
agttaactg caggttcc ggttcaact acttccat cctgggac 700
gtctacggc cagcttcca gtttatctg gtttcaatg agaatccat 750
tactcttc ttcacttt tgggggtg gtcagga cctcgtct 800
cggggggc caggttgg ctgggctg agtcaaat atggtgag 850
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cactcttc cgtttctgg ttatctga ctggcagc tcccaatt 950
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catttgaat gactagag tgggtaga ggcctccg tctgctgt 1100
ggcaggaa gggaaagtg gttcttgg atcaatct ggcagatgg 1150
gcgtgggtg gatttggc caaacaga ggtttggt gtcctggca 1200
gtgaaatcc caggttgt tgggtcag aacaggtt ggggtgct 1250
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aaaaaaaa aaaaaaaaa aaaaaa 1377

<210> 42

400 42

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Ser Pro Pro Leu Asp Asp Asn Lys Ile Pro Ser Leu Cys H₂ Gly
 23 24 25

His Pro Gly Leu Pro Gly Thr Pro Gly His His Gly Ser Glu Gly
3 4 5 6 7 8 9 10

Leu Pro Gly Arg Asp Gly Arg Asp Gly Arg Asp Gly Ala Pro Gly
50 55 60

Ala Pro Gly Glu Lys Gly Glu Gly Gly Arg Pro Gly Leu Pro Gly
65 70 75

Pro Arg Gly Asp Pro Gly Pro Arg Gly Glu Ala Gly Pro Ala Gly
81 82 83 84 85 86 87 88 89 90

Pro Thr Gly Pro Ala Gly Glu Cys Ser Val Pro Pro Arg Ser Ala
gc 100 105

Phe Ser Ala Lys Arg Ser Glu Ser Arg Val Pro Pro Pro Ser Asp
110 115 120

Ala Pro Leu Pro Phe Asp Arg Val Leu Val Asn Glu Gln Gly His
125 130 135

Tyr Asp Ala Val Thr Gly Lys Phe Thr Cys Gln Val Pro Gly Val
140 145 150

Tyr Tyr Phe Ala Val His Ala Thr Val Tyr Arg Ala Ser Leu Gln
145 160 165

Phe Asp Leu Val Lys Asn Gly Gln Ser Ile Ala Ser Phe Phe Gln
110 115 120

Phe Phe Gly Gly Trp Pro Lys Pro Ala Ser Leu Ser Gly Gly Ala
1-5 1-10 195

Met Val Arg Leu Glu Pro Glu Asp Gln Val Trp Val Gln Val Gly
200 205 210

Val Gly Asp Tyr Ile Gly Ile Tyr Ala Ser Ile Lys Thr Asp Ser
215 220 225

Thr Phe Ser Gly Phe Leu Val Tyr Ser Asp Trp His Ser Ser Pro
232 235 240

<210> 43

35

<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 43
tctaggccca gtcagAACCA gggg 24

<210> 44
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 44
agccagcttc gctctcgg 18

<210> 45
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 45
gtctgcgata aggtctgg 18

<210> 46
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 46
gaaagaggca atggattcgc 20

<210> 47
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 47
tacttacact tgcacacaca ccaac 24

<210> 48
<211> 45
<212> DNA
<213> Artificial Sequence

<220>

<221> Synthetic oligonucleotide probe

<400> 42

gagagacacac caactggagg gtccggagta gagagcgccc cgaag 45

<210> 49

<211> 1874

<212> DNA

<213> Homo Sapien.

<400> 43

ctcttttctc caccagccca gctgactcc tggagattgt gaatagctcc 50

atccagctg agaaacagc cgggtgctg agccaggctg tgcacggagc 100

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gagggtatct cctgtctgtg ctcttgccc tcttggtac cactgggca 200

gaggtgtggc caccacagc gcaggagcag gtcggatgg ccggagcct 250

gacagggag gagatcttct tgcctctct cctgcacac cgcctggca 300

gtcgggtcca gcccctgct gctgacatgc ggaggatgga ctggagtga 350

agctggccc aattggcca agccaggcca gccctctgtg gaatcccaac 400

cgcagcctg gcatccacc tctggcgac cctgcacg gactggaac 450

tgcagctgt gccacgggc ttgggtcct ttgttaatt gctcagcta 500

tgggttcacg aggcacgag gtaacggcac cgggagggg atgtgtctg 550

caacggcac tgcacacat acacccagc agtgtggcc actcaagcc 600

agtgagctg tggaggac cgtgtctctg cagcagac aggtatgaa 650

acctctctct gtgtctacc caccacagc aactgagag caaacggaa 700

gacatcac cccataaga agggcgctg gtgttctct tgcacagca 750

gtctctcagg ctgttcaaa gctgggac atgagagg gttctgtgag 800

gtccacagga atcttctcg catgagctgc cagacacat gactctcaa 850

cacacagacc tgcacatgcc actgtccccc tggtaacag gccagatact 900

gcaaatgag gtcacagctc cagtctgtgc accgacgatt cgggagggag 950

gagtgtctgt gctctctgga catcgctac ggggagccc agtgtgccc 1000

caaggtgcat ttctctctcc acacctgtga cctgagpct gacggagct 1050

gcttcctggt gtcttcagag gcagacacat attacagagc caggatgaaa 1100

tctcagagga aaggcgggt gctggcccaq atcaagagcc agaaagtcca 1150

ggacatcctc gecttctatc tgggcgcctt ggagaccacc aacgaggtga 1200
 ctgacagtga cttagagacc aggaacttct ggatecgggt cactacaag 1250
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 caattttgac tttaggnag ctgacaacca cgggtgtgtg tgggtgagt 1350
 ctatcatggg gtttgggaac tgcctggagc tgcagcttc agctgcttc 1400
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 tgcacaggag cactctctt ggtggggccc agggctctga ggttgacca 1500
 catgctctc tgcctggcc tgggagcacc ggtctggtt acgtgtctg 1550
 ctactgtct ggaacaagg ccaggttaag accacatgac tcatgtccaa 1600
 agagtctca gactttgac aatgcagaa gttgggcaga gagaggcagg 1650
 gaggcactg agggccagg agtgagtgtt agaagaagct ggggcccctc 1700
 gctgctttt gattgggaag atgggcttca attagatggc gaaggagagg 1750
 acaccgccag tgggtccaaa aggcctctct ctccacctg gccagaccc 1800
 tatgggacag cggagcttcc ctgtggcatg aacccacgg ggtattaaat 1850
 tatgaatcag ctgaaaaaaa aaaaa 1876

<210> 50
 <211> 455
 <212> FRT
 <213> Homo Sapien

<400> 50
 Met Leu His Pro Gln Thr Ser Pro Gly Arg Gly His Leu Leu Ala
 1 5 10 15
 Val Leu Leu Ala Leu Leu Gly Thr Thr Trp Ala Glu Val Trp Pro
 20 25 30
 Pro Gln Leu Gln Gln Gln Ala Pro Met Ala Gly Ala Leu Asn Arg
 35 40 45
 Lys Glu Ser Phe Leu Leu Leu Ser Leu His Asn Arg Leu Arg Ser
 50 55 60
 Trp Val Gln Pro Pro Ala Ala Arg Met Arg Arg Leu Asp Trp Ser
 65 70 75
 Asp Ser Leu Ala Gln Leu Ala Gln Ala Arg Ala Ala Leu Cys Gly
 80 85 90
 Ile Pro Thr Pro Ser Leu Ala Ser Gly Leu Trp Arg Thr Leu Gln
 95 100 105
 Val Gly Trp Asn Met Gln Leu Leu Pro Ala Gly Leu Ala Ser Phe

110	115	120
Val Glu Val Val Ser Leu Trp Phe Ala	Glu Gly Gln Arg Tyr Ser	
125	130	135
His Ala Ala Gly Glu Cys Ala Arg Asn	Ala Thr Cys Thr His Tyr	
140	145	150
Thr Gln Leu Val Trp Ala Thr Ser Ser	Gln Leu Gly Cys Gly Arg	
155	160	165
His Leu Cys Ser Ala Gly Gln Thr Ala	Ile Glu Ala Phe Val Cys	
170	175	180
Ala Tyr Ser Pro Gly Gly Asn Trp Glu	Val Asn Gly Lys Thr Ile	
185	190	195
Ile Pro Tyr Lys Lys Gly Ala Trp Cys	Ser Leu Cys Thr Ala Ser	
200	205	210
Val Ser Gly Cys Phe Lys Ala Trp Asp	His Ala Gly Gly Leu Cys	
215	220	225
Glu Val Pro Arg Asn Pro Cys Arg Met	Ser Cys Gln Asn His Gly	
230	235	240
Arg Leu Asn Ile Ser Thr Cys His Cys	His Cys Pro Pro Gly Tyr	
245	250	255
Thr Gly Arg Tyr Cys Gln Val Arg Cys	Ser Leu Gln Cys Val His	
260	265	270
Gly Arg Phe Arg Glu Gln Gln Cys Ser	Cys Val Cys Asp Ile Gly	
275	280	285
Tyr Gly Gly Ala Gln Cys Ala Thr Lys	Val His Phe Pro Phe His	
290	295	300
Thr Cys Asp Leu Arg Ile Asp Gly Asp	Cys Phe Met Val Ser Ser	
305	310	315
Glu Ala Asp Thr Tyr Tyr Arg Ala Arg	Met Lys Cys Gln Arg Lys	
320	325	330
Gly Gly Val Leu Ala Gln Ile Lys Ser	Gln Lys Val Gln Asp Ile	
335	340	345
Leu Ala Phe Tyr Leu Gly Arg Leu Glu	Thr Thr Asn Glu Val Thr	
350	355	360
Asp Ser Asp Phe Glu Thr Arg Asn Phe	Trp Ile Gly Leu Thr Tyr	
365	370	375
Lys Thr Ala Lys Asp Ser Phe Arg Trp	Ala Thr Gly Glu His Gln	
380	385	390
Ala Phe Thr Ser Phe Ala Phe Gly Gln	Pro Asp Asn His Gly Leu	
395	400	405

Val Trp Leu Ser Ala Ala Met Gly Phe Gly Asn Cys Val Glu Leu
410 415 420

Gln Ala Ser Ala Ala Phe Asn Trp Asn Asp Gln Arg Cys Lys Thr
425 430 435

Arg Asn Arg Tyr Ile Cys Gln Phe Ala Gln Gln His Ile Ser Arg
440 445 450

Trp Gly Pro Gly Ser
455

<210> 51
<211> 24
<212> DNA
<213> Artificial Sequence

<210>
<212> Synthetic oligonucleotide probe

<400> 51
tjjaatttct ggatcgggc* cacc 24

Q <210> 52
Q <211> 24
Q <212> DNA
Q <213> Artificial Sequence
Q
Q <210>
Q <212> Synthetic oligonucleotide probe

Q <400> 52
Q tngtetgggc caggtggaag agag 24

Q <210> 53
Q <211> 45
Q <212> DNA
Q <213> Artificial Sequence

Q <210>
Q <212> Synthetic oligonucleotide probe

<400> 53
gccaaggact ccttcgctg ggccacagga gaggaccagg ccttc 45

<210> 54
<211> 2331
<212> DNA
<213> Homo Sapien

<400> 54
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tctgtcctg tctgtgggt cgcaggaaga ggcagagag tggggccact 150
cttcggagca ggatggactc agggcccca ggcaagtcag actgttgcag 200

aggetgaaaa ccaaaccttt gatgaragaa ttctcagtga agtctaccat 250
 catttcengt tatgccttca ctacjgttct ctgcagaatg ctgaacagag 300
 ctcttgaaga ccaggacatt gagttctaga tctagattcc agctgcagct 350
 ttcatcaca aattcaatat gtttattgga gacaagggtg atcaggggga 400
 aattacaga agagaaaaa agagtgtga taccgtaaaa gaaaaaagga 450
 ataaaaacac agagaaaaat gaagagaaag gaaatcaat attagaaat 500
 tctcagtga ttcccagaa gacaaagcc ga tttttc tgagttatga 550
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 gccccagca gctgtccggg aactgtggg ttaggtgaa taccctggag 650
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 tcattacaa aattgaaia ttgcacaca taatttttaa acctactgta 800
 gtacaacaag ccaggattgc ccagaatgga attttgggag actttatcat 850
 tagatatgac gtcattagag aacagagcat tggggacatc caggttctaa 900
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 aagaatctgg tatttgtact tgaacagct acttctatcg tgggaaccaa 1000
 actcggccag ac aagatg cctcttcc aattctccat gaactccag 1050
 ccaggaccg ttccagtac attggcttt caacgggat caaggtatg 1100
 aaggaccct taatattgt cactctgac gctctcagg atgggaatt 1150
 atgattcac catarctgac cctcttggg caatcactc aacgggtcc 1200
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 gaaacccgga ggtgttctt catcgtctc ctgacggatg ggaagccac 1300
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caggcctaga ggcatgag agggggacac caaccacac gaggtctct 1800
qagctact caccacaaag gactctga gctcttggct gcaaatcac 1850
gatgaac gg aagaggaggg gctctggcag caggccaggg cctgggtgt 1900
gagctac gc tctctact ccttacct catgaagt aggggacgg 1950
tccacagat gcatggctg gaggagggc acggatgtt ggtgcatg 2000
ggaccgac cgtgtgtga gactgtga gggtgtga cgcagcagg 2050
accttttctc aagaagccaa actctgtcaa aaaaaaaa aacaaaaaa 2100
aaaaaagaca tggagagat ggtttttt cttctacca cctggggata 2150
cgatgagaag atggccact gcaagccagg aagacggcc tccagaca 2200
ccatgtctgc tggaccttg atctggacc tccacctc cagaactgtg 2250
agaaataat gtgttttgtt taagctaaaa aaaaaaaaaa aaaaaaaaaa 2300
aaaaaa aaaa aaaaaaaaaa aaaaaaaaaa a 2331

<210> 55

<211> 694

<212> FRT

<213> Homo Sapien

<400> 55

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Gly	Ser	Gln	Glu	Glu	Ala	Gln	Ser	Trp	Gly	His	Ser	Ser	Gln	Gln
			20						25					30

Asp	Gly	Leu	Arg	Val	Pro	Arg	Gln	Val	Arg	Leu	Leu	Gln	Arg	Leu
			35						40					45

Lys	Thr	Lys	Pro	Leu	Met	Thr	Glu	Phe	Ser	Val	Lys	Ser	Thr	Ile
			50						55					60

Ile	Ser	Arg	Tyr	Ala	Phe	Thr	Thr	Val	Ser	Cys	Arg	Met	Leu	Asn
			65						70					75

Arg	Ala	Ser	Glu	Asp	Gln	Asp	Ile	Glu	Phe	Gln	Met	Gln	Ile	Pro
			80						85					90

Ala	Ala	Ala	Phe	Ile	Thr	Asn	Phe	Thr	Met	Leu	Ile	Gly	Asp	Lys
			95						100					105

Val	Tyr	Gln	Gly	Glu	Ile	Thr	Glu	Arg	Glu	Lys	Lys	Ser	Gly	Asp
			110						115					120

Arg Val Lys Glu Lys Arg Asn Lys Thr Thr Glu Glu Asn Gly Glu
125 130 135

Lys Gly Thr Glu Ile Phe Arg Ala Ser Ala Val Ile Pro Ser Lys
140 145 150

Asp Lys Ala Ala Phe Phe Leu Ser Tyr Glu Glu Leu Leu Gln Arg
155 160 165

Arg Leu Gly Lys Tyr Glu His Ser Ile Ser Val Arg Phe Gln Gln
170 175 180

Leu Ser Gly Arg Leu Ser Val Asp Val Asn Ile Leu Glu Ser Ala
185 190 195

Gly Ile Ala Ser Leu Glu Val Leu Pro Leu His Asn Ser Arg Gln
200 205 210

Arg Gly Ser Gly Arg Gly Glu Asp Asp Ser Gly Pro Pro Pro Ser
215 220 225

Thr Val Ile Asn Gln Asn Glu Thr Phe Ala Asn Ile Ile Phe Lys
230 235 240

Pro Thr Val Val Gln Gln Ala Arg Ile Ala Gln Asn Gly Ile Leu
245 250 255

Gly Asp Phe Ile Ile Arg Tyr Asp Val Asn Arg Glu Gln Ser Ile
260 265 270

Gly Asp Ile Gln Val Leu Asn Gly Tyr Phe Val His Tyr Phe Ala
275 280 285

Pro Lys Asp Leu Pro Pro Leu Pro Lys Asn Val Val Phe Val Leu
290 295 300

Asp Ser Ser Ala Ser Met Val Gly Thr Lys Leu Arg Gln Thr Lys
305 310 315

Asp Ala Leu Phe Thr Ile Leu His Asp Leu Arg Pro Gln Asp Arg
320 325 330

Phe Ser Ile Ile Gly Phe Ser Asn Arg Ile Lys Val Trp Lys Asp
335 340 345

His Leu Ile Ser Val Thr Pro Asp Ser Ile Arg Asp Gly Lys Val
350 355 360

Tyr Ile His His Met Ser Pro Thr Gly Gly Thr Asp Ile Asn Gly
365 370 375

Ala Leu Gln Arg Ala Ile Arg Leu Leu Asn Lys Tyr Val Ala His
380 385 390

Ser Gly Ile Gly Asp Arg Ser Val Ser Leu Ile Val Phe Leu Thr
395 400 405

Asp Gly Lys Pro Thr Val Gly Glu Thr His Thr Leu Lys Ile Leu

410	415	420
Asn Asn Thr Arg Glu Ala Ala Arg Gly Gln Val Cys Ile Phe Thr		
425	430	435
Ile Gly Ile Gly Asn Asp Val Asp Phe Arg Leu Leu Glu Lys Leu		
440	445	450
Ser Leu Glu Asn Cys Gly Leu Thr Arg Arg Val His Gln Gln Glu		
455	460	465
Asp Ala Gly Ser Gln Leu Ile Gly Phe Tyr Asp Glu Ile Arg Thr		
470	475	480
Pro Leu Leu Ser Asp Ile Arg Ile Asp Tyr Pro Pro Ser Ser Val		
485	490	495
Val Gln Ala Thr Lys Thr Leu Phe Pro Asn Tyr Phe Asn Gly Ser		
500	505	510
Glu Ile Ile Ile Ala Gly Lys Leu Val Asp Arg Lys Leu Asp His		
515	520	525
Leu His Val Glu Val Thr Ala Ser Asn Ser Lys Lys Phe Ile Ile		
530	535	540
Leu Lys Thr Asp Val Pro Val Arg Pro Gln Lys Ala Gly Lys Asp		
545	550	555
Val Thr Gly Ser Pro Arg Pro Gly Gly Asp Gly Glu Gly Asp Thr		
560	565	570
Asn His Ile Glu Arg Leu Trp Ser Tyr Leu Thr Thr Lys Glu Leu		
575	580	585
Leu Ser Ser Trp Leu Gln Ser Asp Asp Glu Pro Glu Lys Glu Arg		
590	595	600
Leu Arg Gln Arg Ala Gln Ala Leu Ala Val Ser Tyr Arg Phe Leu		
605	610	615
Thr Pro Phe Thr Ser Met Lys Leu Arg Gly Pro Val Pro Arg Met		
620	625	630
Asp Gly Leu Glu Glu Ala His Gly Met Ser Ala Ala Met Gly Pro		
635	640	645
Glu Pro Val Val Gln Ser Val Arg Gly Ala Gly Thr Gln Pro Gly		
650	655	660
Pro Leu Leu Lys Lys Pro Asn Ser Val Lys Lys Lys Gln Asn Lys		
665	670	675
Thr Lys Lys Arg His Gly Arg Asp Gly Val Phe Pro Leu His His		
680	685	690
Leu Gly Ile Arg		

<210> 56
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<221> Synthetic oligonucleotide probe

<400> 56
gtgggaaaca aatccggga gacc 24

<210> 57
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<221> Synthetic oligonucleotide probe

<400> 57
cacatcgagc gtctctgg 18

<210> 58
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<221> Synthetic oligonucleotide probe

<400> 58
atccctctct tctccggttc atcg 24

<210> 59
<211> 48
<212> DNA
<213> Artificial Sequence

<220>
<221> Synthetic oligonucleotide probe

<400> 59
tggaaggacc acttgatata agtcaactcca gacagcatca gggatggg 48

<210> 60
<211> 141
<212> DNA
<213> Homo Sapien

<400> 60
cggacacatg ggtgaccca catggcgagt gtagtgctga cgagcgatc 50
ccagtgtgga ggggcagcga cggcggcgga ggtcccgga ctccgcttc 100
tgctgttgtt ctctccgga ggggcaactga tcccacagg tgatgggcag 150
aatctgttta cgaaagacgt gacagtgate gagggagagg ttgcgacct 200

cagttggcga gtcaataaga gtgaagactc tgtgattcag ctartgaate 250
 ccaacaggca gaccatttat ttcagggact tcaggccttt gaaggacago 300
 agttttcagt tgttgaattt ttetagaagt gaactcaaa tatcattjac 350
 aaacgtctca attttctgat aaggaagata cttttggca tctctatacg 400
 atcccccaaa ggaaggttac aacacatca caatcctggt cccacacagt 450
 aatctgata tcatatcca gaaagacat ggggtggaa gtgaggagat 500
 tgaagtcaac tgcactgcta tggcagcga gccggccag actatcaggt 550
 ggttcaagg gaacacagag ctaaaaggca aatggagtt ggaagactgg 600
 tcagacatgt acactgtgac caatcagctg atgctgaaag tgcacaagaa 650
 gaagatggg gtcccagtga tctggcaggt ggagacacct gggctcctg 700
 gaaacctgca gaccagcgg tatctagaag tacaatatca gctcagtg 750
 cacatcaga tgaactatcc tctacaaggt ttaaaccggg aaggggaagc 800
 gcttgagtta acatgtgaag ccacggggaa gcccagcct gtgatggtaa 850
 cttgggtgag agtcgatgat gaaatgcctc aacagcaggt actgtctgag 900
 cccacactgt tcatcaaaa cctaaacaaa acacatactg ghaatagag 950
 ctgtcaact tcaacatag tggggaaagc tctctgcat tatatctgt 1000
 atctataga tcccccaaa actatcctc ctccacacac aacacacac 1050
 acacacacaa ccaacacac caccatcctt accatca'ca cagattcccg 1100
 agcaggtgaa gaaggtctga tgaaggcagt gga'cat'cc gtgatcgtg 1150
 ccctcgtggc actgtgata ttcacatgc totgttctc catcatt'ct 1200
 gggcctctatt ttgcagaca taaggtaca tacttactc atgaagcraa 1250
 aggagccgat gacgagcag acgagacac agctataat'c atgcayag 1300
 gaggacagaa caactccgaa gaaaacaaag agtact'cat ctagatcagc 1350
 ctttttgitt caatgaggtg tccactggc ctatattaga tgataaagag 1400
 acagtcata'c tgc 1417

<210> 61
 <211> 440
 <212> PRT
 <213> Homo Sapien

<400> 61
 Met Ala Ser Val Val Leu Pro Ser Gly Ser Gln Cys Ala Ala Ala
 1 5 10 15

Ala Ala Ala Ala Ala Pro Pro Gly Leu Arg Leu Leu Leu Leu Leu
20 25 30

Phe Ser Ala Ala Ala Leu Ile Pro Thr Gly Asp Gly Gln Asn Leu
35 40 45

Phe Thr Lys Asp Val Thr Val Ile Gln Gly Gln Val Ala Thr Ile
50 55 60

Ser Cys Gln Val Asn Lys Ser Asp Asp Ser Val Ile Gln Leu Leu
65 70 75

Asn Pro Asn Arg Gln Thr Ile Tyr Phe Arg Asp Phe Arg Pro Leu
80 85 90

Lys Asp Ser Arg Phe Gln Leu Leu Asn Phe Ser Ser Ser Glu Leu
95 100 105

Lys Val Ser Leu Thr Asn Val Ser Ile Ser Asp Glu Gly Arg Tyr
110 115 120

Phe Cys Gln Leu Tyr Thr Asp Pro Pro Gln Glu Ser Tyr Thr Thr
125 130 135

Ile Thr Val Leu Val Pro Pro Arg Asn Leu Met Ile Asp Ile Gln
140 145 150

Lys Asp Thr Ala Val Glu Gly Glu Glu Ile Glu Val Asn Cys Thr
155 160 165

Ala Met Ala Ser Lys Pro Ala Thr Thr Ile Arg Trp Phe Lys Gly
170 175 180

Asn Thr Gln Leu Lys Gly Lys Ser Gln Val Glu Glu Trp Ser Asp
185 190 195

Met Tyr Thr Val Thr Ser Gln Leu Met Leu Lys Val His Lys Glu
200 205 210

Asp Asp Gly Val Pro Val Ile Cys Gln Val Glu His Pro Ala Val
215 220 225

Thr Gly Asn Leu Gln Thr Gln Arg Tyr Leu Glu Val Gln Tyr Lys
230 235 240

Pro Gln Val His Ile Gln Met Thr Tyr Pro Leu Gln Gly Leu Thr
245 250 255

Arg Glu Gly Asp Ala Leu Glu Leu Thr Cys Gln Ala Ile Gly Lys
260 265 270

Pro Gln Pro Val Met Val Thr Trp Val Arg Val Asp Asp Glu Met
275 280 285

Pro Gln His Ala Val Leu Ser Gly Pro Asn Leu Phe Ile Asn Asn
290 295 300

Leu Asn Lys Thr Asp Asn Gly Thr Tyr Arg Cys Glu Ala Ser Asn

305

310

315

Ile Val Gly Lys Ala His Ser Asp Tyr Met Leu Tyr Val Tyr Asp
320 325 330

Pro Pro Thr Thr Ile Pro Pro Pro Thr Thr Thr Thr Thr Thr Thr
335 340 345

Thr Thr Thr Thr Thr Thr Ile Leu Thr Ile Ile Thr Asp Ser Arg
350 355 360

Ala Gly Glu Glu Gly Ser Ile Arg Ala Val Asp His Ala Val Ile
365 370 375

Gly Gly Val Val Ala Val Val Val Phe Ala Met Leu Cys Leu Leu
380 385 390

Ile Ile Leu Gly Arg Tyr Phe Ala Arg His Lys Gly Thr Tyr Phe
395 400 405

Thr His Glu Ala Lys Gly Ala Asp Asp Ala Ala Asp Ala Asp Thr
410 415 420

Ala Ile Ile Asn Ala Glu Gly Gly Gln Asn Asn Ser Glu Glu Lys
425 430 435

Lys Glu Tyr Phe Ile
440

<210> 62

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 62

ggattctgct gttgctcttc tccg 24

<210> 63

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 63

gtacactgtg accacacagc 20

<210> 64

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 64
atratcacag attcccgagg 20

<210> 65
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<221> Synthetic oligonucleotide probe

<400> 65
ttcaatctcc tcaacttcca ccgc 24

<210> 66
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<221> Synthetic oligonucleotide probe

<400> 66
atagctgtgt ctgcgtctgc tgcg 24

<210> 67
<211> 50
<212> DNA
<213> Artificial Sequence

<220>
<221> Synthetic oligonucleotide probe

<400> 67
caccggcaactg atccccacag ctgatgggca gaatctgttt acgaaadacg 50

<210> 68
<211> 2555
<212> DNA
<213> Homo Sapien

<400> 68
tggcgagggtg gacgcgggact cgaacgcagt tgettcggga cccaggacc 50
cttcggggccc gaaccccccac gaaagactga ggcgcgggccc tgcgccggccc 100
ggctccctgc ggcgcgggccc cctcccgagg caaaagatgt gctccagggt 150
ccctctgatg ctgcgcctgc tctgttact ggcctgggt cctgggtgct 200
agggcttccc atccggtgc cagtgcagcc agccatagac agtctttctg 250
actccccgc aagggacac ggtgccccga gaagtccac ccgacatgt 300
ggggctgtac gtctttgaga accgcattac catgctcgac gcaaggadct 350
ttgcgggctt ggcggggcctg cagctcctgg acctgtcaca gaaccagatc 400

qccagccctgc ggcctgcccgc cctgctgctg ctggaccca qccacacag 450
 cctcctggcc ctggagccgc gcctcctgga cactggccac gtggaggggc 500
 ttgggtggc tggctgggt ctggcgggc tggaggggc gctcttcgc 550
 cgtttggga acccgcgc cctggatctg tccgacacg agctggggc 600
 agtggacat gtgctccgc gctccgggt ctggagggc ctggctgct 650
 ccggacacg cccattccg agctggggc cggaggacat gctgggtg 700
 gctgcctgc aggagctgga tggagggac ctacccctg aggcctggc 750
 tgggacccg tgggcctct tcccccgcct ggggtgctg gtagctgc 800
 gcaacccctt caactggctg tggccctga gctgggttg cccctgggtg 850
 cggagagcc agctacat ggccagccct gaggagagc gctggcatt 900
 ccggccagc agctgggtg ggtgctctt ggagctgac tccggcact 950
 ttggtgccc agccaccac accacagcca cagtggccac caggaggcc 1000
 gtggtgccgc agccacacg cttgctctt agcttggctc ctacctgct 1050
 tagcccccga gctggggca ctgaggccc cagcccgcc tccactgcc 1100
 cccgactgt agggccttc cccagccc agcactgac accctccac 1150
 tccctaatg gggacacat cccctgggc acacggac accgggctg 1200
 cttgtgcgc gaaccttca cgggcctct ctgtgagag cagctgggc 1250
 aggggacac gcccaccc acacagtc cggagggcc acccgctc 1300
 ctgacctgc gcctcagcc ggtgagccc accctctgc gctggggct 1350
 gtagctac ctccaggga gctcctgct gctaggag ctctgctc 1400
 cctatcgca cctatgggc cctgataag ggtgggtac gctggctg 1450
 cctgcctgc tggctgctg cagggtcac cagctgggc ccaagccc 1500
 ttactcctc tgtgctatg ctttggggc cgggggggt cggaggggc 1550
 aggaggtct cggggaggcc cctacacccc cagcgtcca ctccacac 1600
 gcccagtc cccacccc cggaggacac ctgcctcc tcttccgc 1650
 gacctgct cagctctcc tggccgctt ggtgaggt ggggagct 1700
 actgctgc cccgggggc gcctgggc caggggtc gggacagg 1750
 agctgggc cagggtctg gccctggaa ctggaggag tgaaggtcc 1800
 cttgagcca gggccgaag caacagagg cgtggagag gccctgcca 1850

ggggttctga gtgtgaggtt ccaatcatga gcttcccagg gcttgggctc 1900
 caqtcacccc tccacgcaaa gccctacatc taagcccagag agagacaggg 1950
 cagttggggc caggtctctc gcaatgaga tggcagccc cctcctgctg 2000
 ccaacacagc caattctca gtcaccaact cgggaatgtg tgcagacagg 2050
 gctgtgtgac cagagctggg cctcttccc tetggactc gctctctca 2100
 tctctgaaat gctgtggccc agctgagag cctcaactc cccagacccc 2150
 agtgcctatg aggaacagtgt cggccttgc ctcgcacacg tgcagtcctt 2200
 gggcaggcgg ggccttgcca tgtgctggta acgcatgctt gggccttget 2250
 gggctctccc actccaggcg gacctggggg gccagtgaag gaagctcccc 2300
 gaaagagcag agggagagcg ggtaggcggc tgtgtgactc tagtcttggc 2350
 cccaggaagc gaaggaacaa aagaaactgg aaaggaaat gctttaggaa 2400
 catgttttgc ttttttaaaa tatatatata tttataagag atcctttccc 2450
 attttttctg ggaagatggt tttcaaactc agagacaagg actttgggtt 2500
 ttgttaagaca aacgatgata tgaaggcctt ttgtaagaaa aaataaaaaa 2550
 aaaaa 2555

<210> 69
 <211> 598
 <212> PRT
 <213> Homo Sapien

<400> 69
 Met Cys Ser Arg Val Pro Leu Leu Leu Pro Leu Leu Leu Leu Leu
 1 5 10 15
 Ala Leu Gly Pro Gly Val Gln Gly Cys Pro Ser Gly Cys Gln Cys
 20 25 30
 Ser Gln Pro Gln Thr Val Phe Cys Thr Ala Arg Gln Gly Thr Thr
 35 40 45
 Val Pro Arg Asp Val Pro Pro Asp Thr Val Gly Leu Tyr Val Phe
 50 55 60
 Glu Asn Gly Ile Thr Met Leu Asp Ala Ser Ser Phe Ala Gly Leu
 65 70 75
 Pro Gly Leu Gln Leu Leu Asp Leu Ser Gln Asn Gln Ile Ala Ser
 80 85 90
 Leu Arg Leu Pro Arg Leu Leu Leu Leu Asp Leu Ser His Asn Ser
 95 100 105
 Leu Leu Ala Leu Glu Pro Gly Ile Leu Asp Thr Ala Asn Val Glu

110	115	120
Ala Leu Arg Leu Ala Gly Leu Gly Leu Gln Gln Leu Asp Glu Gly		
125	130	135
Leu Phe Ser Arg Leu Arg Asn Leu His Asp Leu Asp Val Ser Asp		
140	145	150
Asn Gln Leu Thr Arg Val Pro Pro Val Ile Arg Gly Leu Arg Gly		
155	160	165
Leu Thr Arg Leu Arg Leu Ala Gly Asn Thr Arg Ile Ala Gln Leu		
170	175	180
Arg Pro Glu Asp Leu Ala Gly Leu Ala Ala Leu Gln Glu Leu Asp		
185	190	195
Val Ser Asn Leu Ser Leu Gln Ala Leu Pro Gly Asp Leu Ser Gly		
200	205	210
Leu Phe Pro Arg Leu Arg Leu Leu Ala Ala Ala Arg Asn Pro Phe		
215	220	225
Asn Cys Val Cys Pro Leu Ser Trp Phe Gly Pro Trp Val Arg Glu		
230	235	240
Ser His Val Thr Leu Ala Ser Pro Glu Glu Thr Arg Cys His Phe		
245	250	255
Pro Pro Lys Asn Ala Gly Arg Leu Leu Leu Glu Leu Asp Tyr Ala		
260	265	270
Asp Phe Gly Cys Pro Ala Thr Thr Thr Thr Ala Thr Val Pro Thr		
275	280	285
Thr Arg Pro Val Val Arg Glu Pro Thr Ala Leu Ser Ser Ser Leu		
290	295	300
Ala Pro Thr Trp Leu Ser Pro Thr Ala Pro Ala Thr Glu Ala Pro		
305	310	315
Ser Pro Pro Ser Thr Ala Pro Pro Thr Val Gly Pro Val Pro Gln		
320	325	330
Pro Gln Asp Cys Pro Pro Ser Thr Cys Leu Asn Gly Gly Thr Cys		
335	340	345
His Leu Gly Thr Arg His His Leu Ala Cys Leu Cys Pro Glu Gly		
350	355	360
Phe Thr Gly Leu Tyr Cys Glu Ser Gln Met Gly Gln Gly Thr Arg		
365	370	375
Pro Ser Pro Thr Pro Val Thr Pro Arg Pro Pro Arg Ser Leu Thr		
380	385	390
Leu Gly Ile Glu Pro Val Ser Pro Thr Ser Leu Arg Val Gly Leu		
395	400	405

Gln Arg Tyr Leu Gln Gly Ser Ser Val Gln Leu Arg Ser Leu Arg
410 415 420

Leu Thr Tyr Arg Asn Leu Ser Gly Pro Asp Lys Arg Leu Val Thr
425 430 435

Leu Arg Leu Pro Ala Ser Leu Ala Glu Tyr Thr Val Thr Gln Leu
440 445 450

Arg Pro Asn Ala Thr Tyr Ser Val Cys Val Met Pro Leu Gly Pro
455 460 465

Gly Arg Val Pro Glu Gly Glu Glu Ala Cys Gly Glu Ala His Thr
470 475 480

Pro Pro Ala Val His Ser Asn His Ala Pro Val Thr Gln Ala Arg
485 490 495

Glu Gly Asn Leu Pro Leu Leu Ile Ala Pro Ala Leu Ala Ala Val
500 505 510

Leu Leu Ala Ala Leu Ala Ala Val Gly Ala Ala Tyr Cys Val Arg
515 520 525

Arg Gly Arg Ala Met Ala Ala Ala Ala Gln Asp Lys Gly Gln Val
530 535 540

Gly Pro Gly Ala Gly Pro Leu Glu Leu Glu Gly Val Lys Val Pro
545 550 555

Leu Glu Pro Gly Pro Lys Ala Thr Glu Gly Gly Gly Glu Ala Leu
560 565 570

Pro Ser Gly Ser Glu Cys Glu Val Pro Leu Met Gly Phe Pro Gly
575 580 585

Pro Gly Leu Gln Ser Pro Leu His Ala Lys Pro Tyr Ile
590 595

<210> 70

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 70

ccctccactg cctccacgac tg 22

<210> 71

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 71
cggttctggg gacgttaggg ctcg 24

<210> 72
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<221> Synthetic oligonucleotide probe

<400> 72
ctgccacccg tccacctgcc tcaat 25

<210> 73
<211> 45
<212> DNA
<213> Artificial Sequence

<220>
<221> Synthetic oligonucleotide probe

<400> 73
aggactgcc accgtccacc tgcctcaatg ggggcacatg ccacc 45

<210> 74
<211> 45
<212> DNA
<213> Artificial Sequence

<220>
<221> Synthetic Oligonucleotide Probe

<400> 74
argcaaaagcc ctacatctaa gccagagaga gacagggcag ctggg 45

<210> 75
<211> 1077
<212> DNA
<213> Homo Sapien

<400> 75
ggcaactagga caacettctt cctttctgca ccaactgcccg taccettacc 50
cgcccgcgcca cttccttgcg accccactct tgaaccacaa gctgttgcca 100
gggtccccag ctcatgccag cctcatctcc ttctttgcta gcccccaaag 150
ggcctccagg caacatgggg ggcacagtcg gagagccggc actctcaatt 200
ggcctctact tcaattgggg ggcacctctg ggggcagtgq cttgtgcaat 250
ggctctgcta acccaaaaaa cagagctgca gajctcagg aaagaggtga 300
gcccgttcca gaggacagga ggcccctccc agaatgggga agggatcccc 350
tggcagagtc tcccggagca gagttccgat gccctgggaag cttgggagaa 400

tggggagaga tccgggaaaa ggagagcagt cctcaccac aaacanaaga 450
 agcagcaetc tgtcttgcac ctgggttccc ttaacgcac ctccaaggat 500
 gactcagtg tgacagaggt catgtggcaa ccagctctt gggtgggag 550
 aggcctacag gcccaagat atgtgtctcc aatccaggat gctgaagttt 600
 atctgtata tagccaggtc ctgtttcaag atgtgatt caaatggt 650
 caagtugtg ctgagagaag ccaaggaagg gaggaact tattcaat 700
 tataagaagt atgcccctcc acccggaacc ggctacaa adctgtata 750
 ggcaggtgt ettcattta caccaagggg atattctga tgcataatt 800
 cccggggcaa gggcgaaact taacctctct ccacatggaa ccttctggg 850
 gtttgtgaaa ctgtgattgt gttataaaaa gtggctccc gcttggaaga 900
 ccagggtggg tataactgg agacagccaa gagctgagta tataaaggag 950
 agggaaatgt caggaacaga ggcattctc tgggtttggc tcccgttcc 1000
 tcaattttcc cttttcattc ccaccccta gactttgatt ttaaggatat 1050
 ctgtcttctg tcccctatgg agctccg 1077

<210> 76
 <211> 250
 <212> PRT
 <213> Homo Sapien

.400> 76
 Met Pro Ala Ser Ser Pro Phe Leu Leu Ala Pro Lys Gly Pro Pro
 1 5 10 15
 Gly Asn Met Gly Gly Pro Val Arg Glu Pro Ala Leu Ser Val Ala
 20 25 30
 Leu Trp Leu Ser Trp Gly Ala Ala Leu Gly Ala Val Ala Cys Ala
 35 40 45
 Met Ala Leu Leu Thr Gln Gln Thr Glu Leu Gln Ser Leu Arg Arg
 50 55 60
 Glu Val Ser Arg Leu Gln Gly Thr Gly Gly Pro Ser Gln Asn Gly
 65 70 75
 Glu Gly Tyr Pro Trp Gln Ser Leu Pro Glu Gln Ser Ser Asp Ala
 80 85 90
 Leu Glu Ala Trp Glu Asn Gly Glu Arg Ser Arg Lys Arg Arg Ala
 95 100 105
 Val Leu Thr Gln Lys Gln Lys Lys Gln His Ser Val Leu His Leu
 110 115 120

Val Pro Ile Asn Ala Thr Ser Lys Asp Asp Ser Asp Val Thr Glu
125 130 135

Val Met Trp Gln Pro Ala Leu Arg Arg Gly Arg Gly Leu Gln Ala
140 145 150

Gln Gly Tyr Gly Val Arg Ile Gln Asp Ala Gly Val Tyr Leu Leu
155 160 165

Tyr Ser Gln Val Leu Phe Gln Asp Val Thr Phe Thr Met Gly Gln
170 175 175

Val Val Ser Arg Glu Gly Gln Gly Arg Gln Glu Thr Leu Phe Arg
185 190 195

Cys Ile Arg Ser Met Pro Ser His Pro Asp Arg Ala Tyr Asn Ser
200 205 210

Cys Tyr Ser Ala Gly Val Phe His Leu His Gln Gly Asp Ile Leu
215 220 225

Ser Val Ile Ile Pro Arg Ala Arg Ala Lys Leu Asn Leu Ser Pro
230 235 240

His Gly Thr Phe Leu Gly Phe Val Lys Leu
245 250

<210> 77
<211> 2849
<212> DNA
<213> Hemo Sapien

<400> 77
caattttctcc ctctcttcttct ttaacttttoga gaaacccgcgc ttcgccttct 50
ggtccagagag acctcggaga ccgcgcgcggg gagacggaga tgetgtgggt 100
ggggggggacc tttgggtgtt cgtaccgcgc cccaccctcc tcttctgcac 150
tgcgcctctc cggagagact ttcccccctgc tctgtttctt tcaaccagtc 200
tgtgcctcgc cccggacctg gcrgggagga ggccttggccg gcgggagatg 250
ctctaggggc ggcacccggag gagcggcccg cgggacggag ggcgccgag 300
gaagatgggc tccgtggac agggactctt gctggcgtac tgcctgctcc 350
ttgcctttac ctctggccta gtctcagtc gtgtgcacca tgtccagggg 400
gaacagcagg agtgggagg gactgaggag ctgcctcgc ctccggacca 450
tgcagagagg gctcagagac aacatgaaaa atacagccc agtcaggagc 500
aggggtctcc tgcctccggg tgcctgcctt gctgtgaccc cgtaccctcc 550
atgtaccggc cgaacgcgtt gccccagatc aacatcaata tcttgaaaag 600
ggagaagggt gaccgcggag atcgaggcct ccaagggaaa tatggcaaaa 650

caggetnagc aggggacagg gggcacactg gacccaaagg gcagaaagg 700
 tccatggggg cccctggggg ggggtggaa ggcactacg cgggttttt 750
 agtgggcccg aagaaagcca tgcacagca ccaactactc cagaaagtga 800
 tttccaaac ggagtttcgt aacctctacg accacttcaa catgttcac 850
 ggaagtct actgtacat ggggggctc tttttttt gctccactt 900
 ccaactctg acccagaag acaactact gcaatctat aatctaat 950
 aggaagtgg gatcttctt ggcaggttg ggcacccag cat atgca 1000
 agccagagcc tcatcttga gctggagag caggacrag tg' ggtacg 1050
 cctctacaag ggcgaacgtg agaacycat ctccag'gag gacttgaca 1100
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<210> 78
 <211> 281
 <212> 1ET
 <213> Homo Sapien

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 20 25 30
 Gln Gly Glu Gln Gln Glu Trp Glu Gly Thr Glu Glu Leu Pro Ser
 35 40 45
 Pro Pro Asp His Ala Glu Arg Ala Glu Glu Gln His Glu Lys Tyr
 50 55 60
 Arg Pro Ser Gln Asp Gln Gly Leu Pro Ala Ser Arg Cys Leu Arg
 65 70 75
 Cys Cys Asp Pro Gly Thr Ser Met Tyr Pro Ala Thr Ala Val Pro
 80 85 90
 Gln Ile Asn Ile Thr Ile Leu Lys Gly Glu Lys Gly Asp Arg Gly
 95 100 105
 Asp Arg Gly Leu Gln Gly Lys Tyr Gly Lys Thr Gly Ser Ala Gly

110	115	120
Ala Arg Gly His Thr Gly Pro Lys Gly Gln Lys Gly Ser Met Gly		
125	130	135
Ala Pro Gly Glu Arg Cys Lys Ser His Tyr Ala Ala Phe Ser Val		
140	145	150
Gly Arg Lys Lys Pro Met His Ser Asn His Tyr Tyr Gln Thr Val		
155	160	165
Ile Phe Asp Thr Glu Phe Val Asn Leu Tyr Asp His Phe Asn Met		
170	175	180
Phe Thr Gly Lys Phe Tyr Cys Tyr Val Pro Gly Leu Tyr Phe Phe		
185	190	195
Ser Leu Asn Val His Thr Trp Asn Gln Lys Glu Thr Tyr Leu His		
200	205	210
Ile Met Lys Asn Glu Glu Glu Val Val Ile Leu Phe Ala Gln Val		
215	220	225
Gly Asp Arg Ser Ile Met Gln Ser Gln Ser Leu Met Leu Glu Leu		
230	235	240
Arg Glu Gln Asp Gln Val Trp Val Arg Leu Tyr Lys Gly Glu Arg		
245	250	255
Glu Asn Ala Ile Phe Ser Glu Glu Leu Asp Thr Tyr Ile Thr Phe		
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<211> 24

<212> INA

<213> Artificial Sequence

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<223> Synthetic oligonucleotide probe

<400> 79

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<210> 80

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 80

ctgaagaagt agaggccggg cacc 24

<210> 81

<211> 45
 <212> DNA
 <213> Artificial Sequence

<221>
 <223> Synthetic oligonucleotide probe

<400> 81
 cccagtgttt gggtagttgt gacccgggtt cctcattgtt cccgg 45

<210> 82
 <211> 2284
 <212> DNA
 <213> Homo Sapien

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<210> 81

<211> 491

<212> PRT

<213> Homo Sapien

<400> 82

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20 25 30

Lys Lys Ser Leu Glu Asp Val Val Ile Asp Ile Gln Ser Ser Leu
35 40 45

Ser Lys Gly Ile Arg Gly Asn Glu Pro Val Tyr Thr Ser Thr Gln
50 55 60

Glu Asp Cys Ile Asn Ser Cys Cys Ser Thr Lys Asn Ile Ser Gly
65 70 75

Asp Lys Ala Cys Asn Leu Met Ile Phe Asp Thr Arg Lys Thr Ala
80 85 90

Arg Gln Pro Asn Cys Tyr Leu Phe Phe Cys Pro Asn Glu Glu Ala
95 100 105

Cys Pro Leu Lys Pro Ala Lys Gly Leu Met Ser Tyr Arg Ile Ile
110 115 120

Thr Asp Phe Pro Ser Leu Thr Arg Asn Leu Pro Ser Gln Glu Leu
125 130 135

Pro Gln Glu Asp Ser Leu Leu His Gly Gln Phe Ser Gln Ala Val
140 145 150

Thr Pro Leu Ala His His His Thr Asp Tyr Ser Lys Pro Thr Asp
155 160 165

Ile Ser Trp Arg Asp Thr Leu Ser Gln Lys Phe Gly Ser Ser Asp
170 175 180

His Leu Glu Lys Leu Phe Lys Met Asp Glu Ala Ser Ala Gln Leu
185 190 195

Leu Ala Tyr Lys Glu Lys Gly His Ser Gln Ser Ser Gln Phe Ser
200 205 210

Ser Asp Gln Glu Ile Ala His Leu Leu Pro Glu Asn Val Ser Ala
215 220 225

Leu Pro Ala Thr Val Ala Val Ala Ser Pro His Thr Thr Ser Ala
230 235 240

Thr Pro Lys Pro Ala Thr Leu Leu Pro Thr Asn Ala Ser Val Thr
245 250 255

Pro Ser Gly Thr Ser Gln Pro Gln Leu Ala Thr Thr Ala Pro Pro
260 265 270

Val Thr Thr Val Thr Ser Gln Pro Pro Thr Thr Leu Ile Ser Thr
275 280 285

Val Phe Thr Arg Ala Ala Ala Thr Leu Gln Ala Met Ala Thr Thr
290 295 300

Ala Val Leu Thr Thr Thr Phe Gln Ala Pro Thr Asp Ser Lys Gly

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Ser Leu Glu Thr Ile Pro Phe Thr Glu Ile Ser Asn Leu Thr Leu		
320	325	330
Asn Thr Gly Asn Val Tyr Asn Pro Thr Ala Leu Ser Met Ser Asn		
335	340	345
Val Glu Ser Ser Thr Met Asn Lys Thr Ala Ser Thr Glu Gly Arg		
350	355	360
Glu Ala Ser Pro Gly Ser Ser Ser Glu Gly Ser Val Pro Glu Asn		
365	370	375
Gln Tyr Gly Leu Pro Phe Glu Lys Thr Leu Leu Ile Gly Ser Leu		
380	385	390
Leu Phe Gly Val Leu Phe Leu Val Ile Gly Leu Val Leu Leu Gly		
395	400	405
Arg Ile Leu Ser Glu Ser Leu Arg Arg Lys Arg Tyr Ser Arg Leu		
410	415	420
Asp Tyr Leu Ile Asn Gly Ile Tyr Val Asp Ile		
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<210> 84

<211> 30

<212> DNA

<213> Artificial Sequence

<220>

<221> Synthetic oligonucleotide probe

<400> 84

aggagaggatt atccttgacc tttgaagacc 30

<210> 85

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<221> Synthetic oligonucleotide probe

<400> 85

gaagcaagtg cccagctc 18

<210> 86

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<221> Synthetic oligonucleotide probe

<400> 86

cgggtccctg ctctttgg 18

<210> 87
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<221> Synthetic oligonucleotide probe

<400> 87
caccgtacat gagagagat taa 24

<210> 88
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
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<400> 88
agtgttaagtc aagctccc 18

<210> 89
<211> 49
<212> DNA
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<220>
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<400> 89
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<210> 90
<211> 957
<212> DNA
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ggagagaggc tatcctaaa gctccagtc ccaaaaggca aaaatgtgac 200
actggaactc cctgcccacc taacacctat gctacaggt tactcagcgg 250
aggtggcaca gcaagtag ccaaaatctg ctttgaggat aacctactta 300
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aactatgtaa ctgggaatgt gacagcaaca caatgttttg atatgtatga 400
aggcgataac tctggaccga tgacaaagtt tcttcagagt gctgctcaca 450
aatccctgct cttcatgggtg acctatgacg acggaagcac aagactgaat 500

aaagatgaca agaattgcat agaagcactt ggaagttaaag aaatcaggaa 550
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 aatagatatt ctgggtgggc tccagagatc caqatagaag gctgcataac 700
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 aacaaatgca gctggaatct ctcaagaate ttattttctt aaatcaaaa 800
 gcccatattt gatgagtatt ttgggtttgt tgtaaaacaa tgaacatttg 850
 ctagtgttat caaatcttgg taagcagtat ttttatacca gtattttatg 900
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 aaaaaaa 957

<210> 91
 <211> 235
 <212> PFT
 <213> Homo Sapien

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 35 40 45
 Ser Ile Gly Glu Arg Pro Val Leu Lys Ala Pro Val Pro Lys Arg 60
 50 55 60
 Gln Lys Cys Asp His Trp Thr Pro Cys Pro Ser Asp Thr Tyr Ala 75
 65 70 75
 Tyr Arg Leu Leu Ser Gly Gly Gly Arg Ser Lys Tyr Ala Lys Ile 90
 80 85 90
 Cys Phe Glu Asp Asn Leu Leu Met Gly Glu Gln Leu Gly Asn Val 105
 95 100 105
 Ala Arg Gly Ile Asn Ile Ala Ile Val Asn Tyr Val Thr Gly Asn 120
 110 115 120
 Val Thr Ala Thr Arg Cys Phe Asp Met Tyr Gln Gly Asp Asn Ser 135
 125 130 135
 Gly Pro Met Thr Lys Phe Ile Gln Ser Ala Ala Pro Lys Ser Leu 150
 140 145 150
 Leu Phe Met Val Thr Tyr Asp Asp Gly Ser Thr Arg Leu Asn Asn 165
 155 160 165

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									190					195	
Leu	Glu	Leu	Pro	Ser	Glu	Ile	Gln	Arg	Glu	Lys	Ile	Asn	His	Ser	
									205					210	
Asp	Ala	Lys	Asn	Asn	Ala	Tyr	Ser	Gly	Trp	Phe	Ala	Glu	Ile	Gln	
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<210> 92
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 <213> Artificial Sequence

<220>
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<400> 92
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<210> 93
 <211> 18
 <212> RNA
 <213> Artificial Sequence

<220>
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<400> 93
 aagttggaa ctcccttc 18

<210> 94
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> Synthetic oligonucleotide probe

<400> 94
 aagattcttg aagcattcca gctg 24

<210> 95
 <211> 47
 <212> DNA
 <213> Artificial Sequence

<220>
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<210> 96
<211> 21
<212> DNA
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ggatctaat tgaagcccat ctcccca 27

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<210> 105

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<223> Synthetic oligonucleotide probe

<400> 106
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<210> 111
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<212> DNA
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<400> 111

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c210> 112
c211> 48
c212> DNA
c213> Artificial Sequence

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(12). Synthetic oligonucleotide probe

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<212> DNA
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4225
4226 Synthetic oligonucleotide probe

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<E11> 48
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20 <211> 48
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40 <213> Artificial Sequence

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-210- 116
-211- 48
-212- DNA
-213- Artificial Sequence

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120% Synthetic oligonucleotide probe

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<211> 48
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<210> 120
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